

**Amendments to the Specification:**

On page 1, under "CROSS REFERENCE TO RELATED APPLICATIONS," please replace the paragraph at line 4 with the following amended paragraph:

~~Not applicable.~~ This application is a national phase application under 35 U.S.C. § 371 of PCT/US00/14829, filed May 26, 2000, which claims the benefit of U.S. Provisional Application No. 60/160,071, filed May 27, 1999.

On page 12, please replace the paragraph beginning at line 4 with the following amended paragraph:

The term "mesothelin" includes reference to a mesothelin protein and fragments thereof which may be present on the surface of cells of a mammal, such as a rat, a mouse, a primate, or, in particular, a human. The preferred nucleic acid and amino acid sequences of mesothelin are as described in PCT published application WO 97/25,068, U.S. Application 08/776,271, now U.S. Patent No. 6,083,502, and U.S. Provisional Application 60/010,166. In addition, *see*, Chang, K. & Pastan, I., *Int. J. Cancer* 57:90 (1994); Chang, K. & Pastan, I., *Proc. Nat'l Acad. Sci. USA* 93:136 (1996); Brinkmann U., *et al.*, *Int. J. Cancer* 71:638 (1997); and Chowdhury, P.S., *et al.*, *Mol. Immunol.* 34:9 (1997). Mesothelin also refers to mesothelin proteins or peptides which remain intracellular, as well as secreted or isolated extracellular protein.

On page 20, please replace the paragraph beginning at line 8 with the following amended paragraph:

Examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1990) *J. Mol. Biol.* 215: 403-410 and Altschuel *et al.* (1977) *Nucleic Acids Res.* 25: 3389-3402, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (~~http://www.~~ which can be

found on the web by entering "www.", followed by: [ncbi.nlm.nih.gov/](http://ncbi.nlm.nih.gov/)). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always  $> 0$ ) and N (penalty score for mismatching residues; always  $< 0$ ). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)).